



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Caras, Ingrid W

(ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

5 (iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/635130
(B) FILING DATE: 19-Mar-1996
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Torchia, PhD., Timothy E.
(B) REGISTRATION NUMBER: 36,700
(C) REFERENCE/DOCKET NUMBER: P1001

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-8674
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

30 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ix) FEATURE:

- (A) NAME/KEY: Extra Cellular Domain
(B) LOCATION: 244-899
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

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(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

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(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNTCTAGAAN TAGTGGATCC CCCCAGGCTG CAGGAATTCC GACGGCCCCCT 50

GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100

CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150

15 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200

TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTC ATG 246

Met

1

GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285

20 Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly

5

10

GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324

Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly

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25 CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363

Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys

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AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402

Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln

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ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441

Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg

55

60

65

CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480

35 Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr

70

75

AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519

	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	Arg	Cys	
	80					85					90			
	GAG	GCA	CCC	CCT	GCC	CCA	AAC	CTC	CTT	CTC	ACT	TGT	GAT	558
5	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
			95					100					105	
	CGC	CCA	GAC	CTG	GAT	CTC	CGC	TTC	ACC	ATC	AAG	TTC	CAG	597
	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	
				110						115				
	GAG	TAT	AGC	CCT	AAT	CTC	TGG	GGC	CAC	GAG	TTC	CGC	TCG	636
10	Glu	Tyr	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	
		120					125					130		
	CAC	CAC	GAT	TAC	TAC	ATC	ATT	GCC	ACA	TCG	GAT	GGG	ACC	675
	His	His	Asp	Tyr	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	
				135					140					
15	CGG	GAG	GGC	CTG	GAG	AGC	CTG	CAG	GGA	GGT	GTG	TGC	CTA	714
	Arg	Glu	Gly	Leu	Glu	Ser	Leu	Gln	Gly	Gly	Val	Cys	Leu	
	145					150					155			
	ACC	AGA	GGC	ATG	AAG	GTG	CTT	CTC	CGA	GTG	GGA	CAA	AGT	753
20	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	Arg	Val	Gly	Gln	Ser	
			160					165					170	
	CCC	CGA	GGA	GGG	GCT	GTC	CCC	CGA	AAA	CCT	GTG	TCT	GAA	792
	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	Val	Ser	Glu	
					175					180				
	ATG	CCC	ATG	GAA	AGA	GAC	CGA	GGG	GCA	GCC	CAC	AGC	CTG	831
25	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	Leu	
		185					190					195		
	GAG	CCT	GGG	AAG	GAG	AAC	CTG	CCA	GGT	GAC	CCC	ACC	AGC	870
	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	
				200					205					
30	AAT	GCA	ACC	TCC	CGG	GGT	GCT	GAA	GGC	CCC	CTG	CCC	CCT	909
	Asn	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	
	210					215					220			
	CCC	AGC	ATG	CCT	GCA	GTG	GCT	GGG	GCA	GCA	GGG	GGG	CTG	948
35	Pro	Ser	Met	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	
			225					230					235	
	GCG	CTG	CTC	TTG	CTG	GGC	GTG	GCA	GGG	GCT	GGG	GGT	GCC	987
	Ala	Leu	Leu	Leu	Leu	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	
					240					245				
	ATG	TGT	TGG	CGG	AGA	CGG	CGG	GCC	AAG	CCT	TCG	GAG	AGT	1026

	Met	Cys	Trp	Arg	Arg	Arg	Arg	Ala	Lys	Pro	Ser	Glu	Ser	
	250						255					260		
	CGC	CAC	CCT	GGT	CCT	GGC	TCC	TTC	GGG	AGG	GGA	GGG	TCT	1065
5	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	Arg	Gly	Gly	Ser	
				265					270					
	CTG	GGC	CTG	GGG	GGT	GGA	GGT	GGG	ATG	GGA	CCT	CGG	GAG	1104
	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	Arg	Glu	
	275					280					285			
	GCT	GAG	CCT	GGG	GAG	CTA	GGG	ATA	GCT	CTG	CGG	GGT	GGC	1143
10	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
			290					295					300	
	GGG	GCT	GCA	GAT	CCC	CCC	TTC	TGC	CCC	CAC	TAT	GAG	AAG	1182
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	
				305						310				
15	GTG	AGT	GGT	GAC	TAT	GGG	CAT	CCT	GTG	TAT	ATC	GTG	CAG	1221
	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	
		315					320					325		
	GAT	GGG	CCC	CCC	CAG	AGC	CCT	CCA	AAC	ATC	TAC	TAC	ACA	1260
20	Asp	Gly	Pro	Pro	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	
				330					335					
	TCG	ATT	TCT	GTG	TTG	GAG	TGG	CCC	ATA	TTG	CAT	ACG	ATA	1299
	Ser	Ile	Ser	Val	Leu	Glu	Trp	Pro	Ile	Leu	His	Thr	Ile	
	340					345					350			
	CAA	CTG	TTT	TTC	ATG	CGA	TCC	AAG	TGC	TCC	CGT	GTC	ACT	1338
25	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	Cys	Ser	Arg	Val	Thr	
			355					360					365	
	ACA	TTC	TTA	TTT	CCT	GTG	CAA	GTT	ATT	ACG	ACA	TCG	ACT	1377
	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	Thr	Ser	Thr	
					370					375				
30	TGC	CGG	ATG	ACT	TCA	TTT	AGC	TTT	ACC	ACC	CTG	AAC	CCA	1416
	Cys	Arg	Met	Thr	Ser	Phe	Ser	Phe	Thr	Thr	Leu	Asn	Pro	
		380					385					390		
	TCC	ATG	CAG	GCC	TGC	AGA	GCA	CAG	ATG	GGG	GAA	TTC	CGA	1455
35	Ser	Met	Gln	Ala	Cys	Arg	Ala	Gln	Met	Gly	Glu	Phe	Arg	
				395					400					
	ATC	AGA	TGG	TGT	TTC	TGG	GGG	GAC	AGG	ATC	CTG	GGT	ACG	1494
	Ile	Arg	Trp	Cys	Phe	Trp	Gly	Asp	Arg	Ile	Leu	Gly	Thr	
	405					410					415			
	GCT	CTG	TTT	GTG	CTT	GTG	CTT	ATT	CTT	CTT	CTT	GGG	AGG	1533

Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
 420 425 430

CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
 5 435 440

AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
 445 450 455

ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660

10 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710

CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760

TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810

CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGAATTCGA TATCAAGCTT 1860

ATCGATACCG TCGACCT 1877

15 (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
 1 5 10 15

Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
 20 25 30

25 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
 35 40 45

Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
 50 55 60

30 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
 65 70 75

Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
 80 85 90

Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
 95 100 105

	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
					110					115					120	
	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
					125					130					135	
5	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
					140					145					150	
	Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
					155					160					165	
10	Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
					170					175					180	
	Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
					185					190					195	
	Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
					200					205					210	
15	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
					215					220					225	
	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
					230					235					240	
20	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
					245					250					255	
	Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
					260					265					270	
	Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
					275					280					285	
25	Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
					290					295					300	
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
					305					310					315	
30	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	
					320					325					330	
	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	Ser	Ile	Ser	Val	Leu	Glu	
					335					340					345	
	Trp	Pro	Ile	Leu	His	Thr	Ile	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	
					350					355					360	
35	Cys	Ser	Arg	Val	Thr	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	

	365	370	375
	Thr Ser Thr Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn		
	380	385	390
5	Pro Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg Ile		
	395	400	405
	Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr Ala Leu Phe		
	410	415	420
	Val Leu Val Leu Ile Leu Leu Leu Gly Arg Leu Asn Met His Gln		
	425	430	435
10	Thr Thr Leu Leu Arg Gln Arg Ala Ser Val Glu Ala Glu Ala Gly		
	440	445	450
	Gln His Gly Pro Leu		
	455		

(2) INFORMATION FOR SEQ ID NO:3:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2380 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GNTCTAGAA TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCCT 50

GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100

CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150

CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200

25 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTCATGGGGC 250

CCCCCATTC TGGGCCGGGG GGCCTGCGAG TCGGGGCCCT GCTGCTGCTG 300

GGGGTTTTGG GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350

CTCGGCGAAT AAGAGGTTCC AGGCAGAGGG TGGTTATGTG CTGTACCCTC 400

AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCC GCCTCCTGGC 450

30 CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500

TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA 550

CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600
 TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650
 CATCATTGCC ACATCGGATG GGACCCGGGA GGGCCTGGAG AGCCTGCAGG 700
 GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750
 5 AGTCCCCGAG GAGGGGCTGT CCCCCGAAAA CCTGTGTCTG AAATGCCCCAT 800
 GGAAAGAGAC CGAGGGGCGAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC 850
 TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900
 CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950
 GCTGCTCTTG CTGGGCGTGG CAGGGGCTGG GGGTGCCATG TGTGCGCGGA 1000
 10 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC 1050
 GGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG 1100
 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGT GCGGGGGCTG 1150
 CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGAATATGGG 1200
 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT 1250
 15 CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC 1300
 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA 1350
 ACATCTCGGC CCCCTGTGCC CCCCAGCCC CTTCACTCCT CCCGGCTGCT 1400
 GTCCCTCGTCT CCACTTTTAG GATTCCTTAG GATTCCCACT GCCCCACTTC 1450
 CTGCCCCCCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG 1500
 20 ATCCTTTTTT CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550
 ACCCAGGCAT CTTGTGCCCC CTCACCCACC CAGAGCTAGG GCGGGGAACA 1600
 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT 1650
 CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700
 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT 1750
 25 ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTTCTCCC 1800
 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850

TCTGCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCAG 1900
 CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950
 ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000
 AGAAGAAGTG TCCCGTTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050
 5 TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGGCCA CTTGGGACCG 2100
 GAAGTGA CTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150
 TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTTCATCCAG 2200
 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAAC TCAA 2250
 GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300
 10 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACCT 2350
 ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 340 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Gly	Pro	Pro	His	Ser	Gly	Pro	Gly	Gly	Val	Arg	Val	Gly	Ala	
	1				5					10					15	
20	Leu	Leu	Leu	Leu	Gly	Val	Leu	Gly	Leu	Val	Ser	Gly	Leu	Ser	Leu	
					20					25					30	
	Glu	Pro	Val	Tyr	Trp	Asn	Ser	Ala	Asn	Lys	Arg	Phe	Gln	Ala	Glu	
					35					40					45	
25	Gly	Gly	Tyr	Val	Leu	Tyr	Pro	Gln	Ile	Gly	Asp	Arg	Leu	Asp	Leu	
					50					55					60	
	Leu	Cys	Pro	Arg	Ala	Arg	Pro	Pro	Gly	Pro	His	Ser	Ser	Pro	Asn	
					65					70					75	
	Tyr	Glu	Phe	Tyr	Lys	Leu	Tyr	Leu	Val	Gly	Gly	Ala	Gln	Gly	Arg	
					80					85					90	
30	Arg	Cys	Glu	Ala	Pro	Pro	Ala	Pro	Asn	Leu	Leu	Leu	Thr	Cys	Asp	
					95					100					105	

	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
					110					115					120	
	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
					125					130					135	
5	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
					140					145					150	
	Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
					155					160					165	
10	Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
					170					175					180	
	Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
					185					190					195	
	Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
					200					205					210	
15	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
					215					220					225	
	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
					230					235					240	
20	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
					245					250					255	
	Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
					260					265					270	
	Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
					275					280					285	
25	Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
					290					295					300	
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
					305					310					315	
30	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	
					320					325					330	
	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Lys	Val						
					335					340						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 454 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 GCCGACGCTG TGAGGCACCC CCTGCCCCAA ACCTCCTTCT CACTTGTGAT 50
CGCCCAGACC TGGATCTCCG CTTACCATC AAGTTCCAGG AGTATAGCCC 100
TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTG 150
CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG 200
TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA 250
10 GGAGGGGCTG TCCCCCGAAA ACCTGTGTCT GAAATGCCCA TGGAAAGAGA 300
CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG 350
TGACCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400
CCCTTTCCCA GCATTGCNTG CANTTGGTTN GGGGCAGCAN GGGGGNGTTT 450
TGGC 454

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30 GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50

CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50

10 TTCCATGGGC 60



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: Caras, Ingrid W
- (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 460 Point San Bruno Blvd
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/635130
 - (B) FILING DATE: 19-Mar-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Torchia, PhD., Timothy E.
 - (B) REGISTRATION NUMBER: 36,700
 - (C) REFERENCE/DOCKET NUMBER: P1001
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 415/225-8674
 - (B) TELEFAX: 415/952-9881
 - (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1877 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Extra Cellular Domain
- (B) LOCATION: 244-899
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

(A) NAME/KEY: Transmembrane Domain

(B) LOCATION: 901-978

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(ix) FEATURE:

(A) NAME/KEY: signal peptide

(B) LOCATION: 244-321

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNTCTAGAA TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCT 50

GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100

CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150

15 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200

TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTC ATG 246

Met

1

GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285

20 Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly

5

10

GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324

Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly

15

20

25

25 CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363

Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys

30

35

40

AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402

Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln

30

45

50

ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441

Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg

55

60

65

CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480

35 Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr

70

75

AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519

Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
80 85 90

GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
5 95 100 105

CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
110 115

GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
10 Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
120 125 130

CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr
135 140

CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
15 Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
145 150 155

ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
20 Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
160 165 170

CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
175 180

ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
25 Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
185 190 195

GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
200 205

AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
30 Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
210 215 220

CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
35 Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
225 230 235

GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala
240 245

ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026

	Met	Cys	Trp	Arg	Arg	Arg	Arg	Ala	Lys	Pro	Ser	Glu	Ser	
	250						255					260		
	CGC	CAC	CCT	GGT	CCT	GGC	TCC	TTC	GGG	AGG	GGA	GGG	TCT	1065
5	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	Arg	Gly	Gly	Ser	
	265						270							
	CTG	GGC	CTG	GGG	GGT	GGA	GGT	GGG	ATG	GGA	CCT	CGG	GAG	1104
	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	Arg	Glu	
	275					280					285			
	GCT	GAG	CCT	GGG	GAG	CTA	GGG	ATA	GCT	CTG	CGG	GGT	GGC	1143
10	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
	290						295					300		
	GGG	GCT	GCA	GAT	CCC	CCC	TTC	TGC	CCC	CAC	TAT	GAG	AAG	1182
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	
				305				310						
15	GTG	AGT	GGT	GAC	TAT	GGG	CAT	CCT	GTG	TAT	ATC	GTG	CAG	1221
	Val	Ser	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	
	315					320					325			
	GAT	GGG	CCC	CCC	CAG	AGC	CCT	CCA	AAC	ATC	TAC	TAC	ACA	1260
20	Asp	Gly	Pro	Pro	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	
			330				335							
	TCG	ATT	TCT	GTG	TTG	GAG	TGG	CCC	ATA	TTG	CAT	ACG	ATA	1299
	Ser	Ile	Ser	Val	Leu	Glu	Trp	Pro	Ile	Leu	His	Thr	Ile	
	340				345					350				
	CAA	CTG	TTT	TTC	ATG	CGA	TCC	AAG	TGC	TCC	CGT	GTC	ACT	1338
25	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	Cys	Ser	Arg	Val	Thr	
	355						360					365		
	ACA	TTC	TTA	TTT	CCT	GTG	CAA	GTT	ATT	ACG	ACA	TCG	ACT	1377
	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	Thr	Ser	Thr	
				370			375							
30	TGC	CGG	ATG	ACT	TCA	TTT	AGC	TTT	ACC	ACC	CTG	AAC	CCA	1416
	Cys	Arg	Met	Thr	Ser	Phe	Ser	Phe	Thr	Thr	Leu	Asn	Pro	
	380					385					390			
	TCC	ATG	CAG	GCC	TGC	AGA	GCA	CAG	ATG	GGG	GAA	TTC	CGA	1455
35	Ser	Met	Gln	Ala	Cys	Arg	Ala	Gln	Met	Gly	Glu	Phe	Arg	
			395				400							
	ATC	AGA	TGG	TGT	TTC	TGG	GGG	GAC	AGG	ATC	CTG	GGT	ACG	1494
	Ile	Arg	Trp	Cys	Phe	Trp	Gly	Asp	Arg	Ile	Leu	Gly	Thr	
	405				410					415				
	GCT	CTG	TTT	GTG	CTT	GTG	CTT	ATT	CTT	CTT	CTT	GGG	AGG	1533

Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
420 425 430

CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala

5 435 440

AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
445 450 455

ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660

10 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC COTGGCAGGT 1710

CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCG ACAGAATTTA 1760

TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCTG TGCTGCCTGT 1810

CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAAATTCGA TATCAAGCTT 1860

ATCGATACCG TCGACCT 1877

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
1 5 10 15

Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
20 25 30

25 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
35 40 45

Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
50 55 60

30 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
65 70 75

Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
80 85 90

Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
95 100 105

	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
					110					115					120	
	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
					125					130					135	
5	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
					140					145					150	
	Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
					155					160					165	
10	Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
					170					175					180	
	Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
					185					190					195	
	Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
					200					205					210	
15	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
					215					220					225	
	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
					230					235					240	
20	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
					245					250					255	
	Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
					260					265					270	
	Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
					275					280					285	
25	Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
					290					295					300	
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
					305					310					315	
30	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	
					320					325					330	
	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Thr	Ser	Ile	Ser	Val	Leu	Glu	
					335					340					345	
	Trp	Pro	Ile	Leu	His	Thr	Ile	Gln	Leu	Phe	Phe	Met	Arg	Ser	Lys	
					350					355					360	
35	Cys	Ser	Arg	Val	Thr	Thr	Phe	Leu	Phe	Pro	Val	Gln	Val	Ile	Thr	

365

370

375

Thr Ser Thr Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn
380 385 390

5 Pro Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg Ile
395 400 405

Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr Ala Leu Phe
410 415 420

Val Leu Val Leu Ile Leu Leu Leu Gly Arg Leu Asn Met His Gln
425 430 435

10 Thr Thr Leu Leu Arg Gln Arg Ala Ser Val Glu Ala Glu Ala Gly
440 445 450

Gln His Gly Pro Leu
455

(2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GNTCTAGAA TAGTGGATCC CCCC GGGCTG CAGGAATTCC GACGGCCCCT 50
GGAAGGGCTC TGGTGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
25 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CTTGGCGGG GTCATGGGGC 250
CCCCCATTC TGGGCCGGGG GGCCTGCGAG TCGGGGCCCT GCTGCTGCTG 300
GGGGTTTGG GGCTGGTGTC TGGGCTCAGC CTGGAGCCTG TCTACTGGAA 350
CTCGCGGAAT AAGAGGTTCC AGGCAGAGGG TGTTATGTG CTGTACCCTC 400
AGATCGGGGA CCGGCTAGAC CTGCTCTGCC CCCGGGCCCC GCCTCCTGGC 450
30 CCTCACTCCT CTCCTAATTA TGAGTTCTAC AAGCTGTACC TGGTAGGGGG 500
TGCTCAGGGC CGGCGCTGTG AGGCACCCCC TGCCCCAAAC CTCCTTCTCA 550

CTTGTGATCG CCCAGACCTG GATCTCCGCT TCACCATCAA GTTCCAGGAG 600
 TATAGCCCTA ATCTCTGGGG CCACGAGTTC CGCTCGCACC ACGATTACTA 650
 CATCATTGCC ACATCGGATG GGACCCGGGA GGGCCTGGAG AGCCTGCAGG 700
 GAGGTGTGTG CCTAACCAGA GGCATGAAGG TGCTTCTCCG AGTGGGACAA 750
 5 AGTCCCCGAG GAGGGGCTGT CCCCCGAAAA CCTGTGTCTG AAATGCCCCAT 800
 GGAAAGAGAC CGAGGGGCGAG CCCACAGCCT GGAGCCTGGG AAGGAGAACC 850
 TGCCAGGTGA CCCCACCAGC AATGCAACCT CCCGGGGTGC TGAAGGCCCC 900
 CTGCCCCCTC CCAGCATGCC TGCAGTGGCT GGGGCAGCAG GGGGGCTGGC 950
 GCTGCTCTTG CTGGGCGTGG CAGGGGCTGG GGGTGCCATG TGTGCGCGGA 1000
 10 GACGGCGGGC CAAGCCTTCG GAGAGTCGCC ACCCTGGTCC TGGCTCCTTC 1050
 GGGAGGGGAG GGTCTCTGGG CCTGGGGGGT GGAGGTGGGA TGGGACCTCG 1100
 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGT GGCGGGGCTG 1150
 CAGATCCCCC CTTCTGCCCC CACTATGAGA AGGTGAGTGG TGAATATGGG 1200
 CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT 1250
 15 CTACTACAAG GTATGAGGGC TCCTCTCACG TGGCTATCCT GAATCCAGCC 1300
 CTTCTTGGGG TGCTCCTCCA GTTTAATTC TGGTTTGAGG GACACCTCTA 1350
 ACATCTCGGC CCCCTGTGCC CCCCAGCCC CTTCACTCCT CCCGGCTGCT 1400
 GTCCCTCGTCT CCACTTTTAG GATTTCCTTAG GATTCCCACT GCCCCACTTC 1450
 CTGCCCCTCC GTTTGGCCAT GGGTGCCCCC CTCTGTCTCA GTGTCCCTGG 1500
 20 ATCCTTTTTT CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550
 ACCCAGGCAT CTTGTGCCCC CTCACCCACC CAGAGCTAGG GGCGGGAACA 1600
 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT 1650
 CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700
 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT 1750
 25 ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTTCTCCC 1800
 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850

TCTGCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCAG 1900

CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950

ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000

AGAAGAAGTG TCCCGTTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050

5 TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGGCCA CTTGGGACCG 2100

GAAGTGA CTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150

TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTTCATCCAG 2200

GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACCTCAA 2250

GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300

10 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACCTT 2350

ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 340 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
1 5 10 15

20 Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
20 25 30

Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
35 40 45

25 Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
50 55 60

Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
65 70 75

Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
80 85 90

30 Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
95 100 105

	Arg	Pro	Asp	Leu	Asp	Leu	Arg	Phe	Thr	Ile	Lys	Phe	Gln	Glu	Tyr	
					110					115					120	
	Ser	Pro	Asn	Leu	Trp	Gly	His	Glu	Phe	Arg	Ser	His	His	Asp	Tyr	
					125					130					135	
5	Tyr	Ile	Ile	Ala	Thr	Ser	Asp	Gly	Thr	Arg	Glu	Gly	Leu	Glu	Ser	
					140					145					150	
	Leu	Gln	Gly	Gly	Val	Cys	Leu	Thr	Arg	Gly	Met	Lys	Val	Leu	Leu	
					155					160					165	
	Arg	Val	Gly	Gln	Ser	Pro	Arg	Gly	Gly	Ala	Val	Pro	Arg	Lys	Pro	
10					170					175					180	
	Val	Ser	Glu	Met	Pro	Met	Glu	Arg	Asp	Arg	Gly	Ala	Ala	His	Ser	
					185					190					195	
	Leu	Glu	Pro	Gly	Lys	Glu	Asn	Leu	Pro	Gly	Asp	Pro	Thr	Ser	Asn	
					200					205					210	
15	Ala	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Met	
					215					220					225	
	Pro	Ala	Val	Ala	Gly	Ala	Ala	Gly	Gly	Leu	Ala	Leu	Leu	Leu	Leu	
					230					235					240	
	Gly	Val	Ala	Gly	Ala	Gly	Gly	Ala	Met	Cys	Trp	Arg	Arg	Arg	Arg	
20					245					250					255	
	Ala	Lys	Pro	Ser	Glu	Ser	Arg	His	Pro	Gly	Pro	Gly	Ser	Phe	Gly	
					260					265					270	
	Arg	Gly	Gly	Ser	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Met	Gly	Pro	
					275					280					285	
25	Arg	Glu	Ala	Glu	Pro	Gly	Glu	Leu	Gly	Ile	Ala	Leu	Arg	Gly	Gly	
					290					295					300	
	Gly	Ala	Ala	Asp	Pro	Pro	Phe	Cys	Pro	His	Tyr	Glu	Lys	Val	Ser	
					305					310					315	
	Gly	Asp	Tyr	Gly	His	Pro	Val	Tyr	Ile	Val	Gln	Asp	Gly	Pro	Pro	
30					320					325					330	
	Gln	Ser	Pro	Pro	Asn	Ile	Tyr	Tyr	Lys	Val						
					335					340						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 454 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 GCCGACGCTG TGAGGCACCC CCTGCCCCAA ACCTCCTTCT CACTTGTGAT 50
CGCCCAGACC TGGATCTCCG CTTACCATC AAGTTCCAGG AGTATAGCCC 100
TAATCTCTGG GGCCACGAGT TCCGCTCGCA CCACGATTAC TACATCATTTG 150
CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG 200
TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA 250
10 GGAGGGGCTG TCCCCCGAAA ACCTGTGTCT GAAATGCCCA TGGAAAGAGA 300
CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG 350
TGACCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA 400
CCCTTTCCCA GCATTGCNTG CANTTGGTTN GGGGCAGCAN GGGGGNGTTT 450
TGGC 454

15 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30 GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50

CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 60 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50

10 TTCCATGGGC 60

File DKB2: [MANDL] HS006163.EMEST1;1
 ID HS006163 standard; RNA; EST; 454 BP.
 XX
 AC H10006;
 XX
 NI g874828
 XX
 DT 02-JUL-1995 (Rel. 44, Created)
 DT 02-JUL-1995 (Rel. 44, Last updated, Version 1)
 XX
 DE ym02e11.r1 Homo sapiens cDNA clone 46610 5' similar to contains Alu
 DE repetitive element;.
 XX
 KW EST.
 XX
 OS Homo sapiens (human)
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP 1-454
 RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
 RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
 RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
 RA Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
 RT "The WashU-Merck EST Project";
 RL Unpublished.
 XX
 CC GDB: G00-419-151 Contact: Wilson RK WashU-Merck EST Project
 CC Washington University School of Medicine 4444 Forest Park Parkway,
 CC Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
 CC Email: est@watson.wustl.edu High quality sequence stops: 313
 CC Source: IMAGE Consortium, LLNL This clone is available royalty-free
 CC through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
 CC for further information. NCBI gi: 874828

XX
 FH Key Location/Qualifiers
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 FT source 1. .454
 FT /organism="Homo sapiens"
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Hs006163 Length: 454 August 19, 1997 11:01 Type: N Check: 5608 ..

1 GCCGACGCTG TGAGGCACCC CCTGCCCAA ACCTCCTTCT CACTTGTGAT
 51 CGCCCAGACC TGGATCTCCG CTTCAACATC AAGTTCCAGG AGTATAGCCC
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 151 CCACATCGGA TGGGACCCGG GAGGCCTGGG AGAGCCTGCA GGGAAGTGTG
 201 TGCCTAACCA GAGGCATGAA GGTGCTTCTC CGAGTNGGAC AAAGTCCCGA

251 GGAGGGGCTG TCCC AAA ACCTGTGTCT GAAATGCCCA GGAAAGAGA
301 CCGAGGGGCA GCCCACAGCC TGGGAGCCTG GGGAAGGAGA ACCTGCCAGG
351 TGACCCCACC AGCAATNCAA CCTTCCGGGG TTGCTTGAAG GGCCCCTTGA
401 CCCTTTCCCA GCATTGCNTG CANTTGGTTN GGGGCAGCAN GGGGGNGTTT
451 TGGC

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D HSU57001 standard; RNA; HUM; 1708 BP.

XX
C U57001;

XX
II g1469781

XX
DT 31-JUL-1996 (Rel. 48, Created)

DT 31-JUL-1996 (Rel. 48, Last updated, Version 1)

XX
DE Human ligand for eph-related receptor tyrosine kinases (EPLG8)
DE mRNA, complete cds.

XX
KW

XX

OS Homo sapiens (human)

OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-1708

RA Cerretti D.P.;

RT "LERK-8, a ligand for the eph-related receptor tyrosine kinases";

RL Unpublished.

XX

RN [2]

RP 1-1708

RA Cerretti D.P.;

RT

RL Submitted (29-APR-1996) to the EMBL/GenBank/DDBJ databases.

RL Douglas P. Cerretti, Molecular Biology, Immunex Corp., 51

RL University St., Seattle, WA 98101, USA

XX

DR SPTREMBL; Q15768; Q15768.

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FH Key Location/Qualifiers

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FT source 1. .1708

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201 CCCTGGAAGG GCTCTGGTGG GGCTGAGCGC TCTGCCGCGG GGGCGCGGGC
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551 CCTCAGATCG GGGACCGGCT AGACCTGCTC TGCCCCCGGG CCCGGCCTCC
601 TGGCCCTCAC TCCTCTCCTA ATTATGAGTT CTACAAGCTG TACCTGGTAG
651 GGGGTGCTCA GGGCCGGCGC TGTGAGGCAC CCCCTGCCCC AAACCTCCTT
701 CTCACTTGTG ATCGCC CAGA CCTGGATCTC CGCTTCACCA TCAAGTTCCA
751 GGAGTATAGC CCTAATCTCT GGGGCCACGA GTTCCGCTCG CACCACGATT

801 ACTACATCAT TGCCACATCG GATGGGACCC GGGAGGGCCT GGAGAGCCTG
851 CAGGGAGGTG TGTGCCTAAC CAGAGGCATG AAGGTGCTTC TCCGAGTGGG
901 ACAAAGTCCC CGAGGAGGGG CTGTCCCCCG AAAACCTGTG TCTGAAATGC
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